

DESeq differential gene expression output table column definitions

ID:

The Gene ID listed in the annotation file

Log2FoldChange

The Log2 fold change of the normalized mean hit counts. The formula is:

$\text{Log}_2(\text{Group 2 mean normalized counts}/\text{Group 1 mean normalized counts}) = \text{Log}_2\text{FoldChange}$

Group 1: First group listed in the testCondition.txt file

Group 2: Second group listed in the testCondition.txt file

pvalue

The Wald test p-value

padj

The Benjamini-Hochberg adjusted p-value

[Sample Name]

(For each sample) the normalized hit counts for the gene

Gene.name

If available, the Gene Name/Symbol for each Gene ID listed in the annotation file